

## Additional File 3

Tables S1-3 are combined in Additional File 2 (XLS format):

**Table S1. Full screen results**

**Table S2. Target gene analysis (siRNA knockdown efficiencies)**

**Table S3. Detailed analysis of 193 screen hits**

**Table S4. *TGFBR2* is the most significantly off-targeted gene (guide strand).**

rank	gene	UTR length	count in hits	count in control	enrichment	p-value	Ensembl ID
1	<b><i>TGFBR2</i></b>	2535	78	729	2.674897	<b>6.42E-12</b>	ENST00000295754
2	<b><i>CD248</i></b>	267	19	92	5.163043	<b>1.14E-03</b>	ENST00000311330
3	<b><i>C3orf52</i></b>	563	26	182	3.571429	<b>2.63E-03</b>	ENST00000480282
4	<b><i>GALE</i></b>	345	21	125	4.2	<b>4.82E-03</b>	ENST00000456977
5	<b><i>C9orf107</i></b>	201	16	71	5.633803	<b>5.31E-03</b>	ENST00000374801
6	<b><i>SBF1</i></b>	391	22	140	3.928571	<b>6.74E-03</b>	ENST00000356279
7	<b><i>TYMP</i></b>	500	24	173	3.468208	<b>1.44E-02</b>	ENST00000426603
8	<b><i>KCNC2</i></b>	1124	35	338	2.588757	<b>1.87E-02</b>	ENST00000298972
9	<b><i>CSN3</i></b>	201	14	68	5.147059	8.52E-02	ENST00000304954
10	<b><i>SYPL1</i></b>	505	21	152	3.453947	8.68E-02	ENST00000470347

The siRNA seed matches with 3'UTRs of all genes were compared between the top 200 and a control group of non-hits (screen ranks 12,001-17,000). The significance of enrichment was highest for *TGFBR2* (Fisher's exact test).

**Table S5. *TGFBR2* is among the most off-targeted gene (passenger strand).**

rank	gene	UTR length	count in hits	count in control	enrichment	p-value	Ensembl ID
1	<b><i>C17orf95</i></b>	193	10	54	4.62963	<b>5.53E+00</b>	ENST00000317409
2	<b><i>MAP3K13</i></b>	220	11	74	3.716216	<b>1.44E+01</b>	ENST00000454237
3	<b><i>CDK15</i></b>	805	27	329	2.051672	<b>1.79E+01</b>	ENST00000451080
4	<b><i>ODZ2</i></b>	1347	30	389	1.928021	<b>2.26E+01</b>	ENST00000403607
5	<b><i>CETN1</i></b>	597	21	231	2.272727	<b>2.38E+01</b>	ENST00000327228
6	<b><i>TET3</i></b>	395	14	124	2.822581	<b>3.04E+01</b>	ENST00000409262
7	<b><i>TGFBR2</i></b>	2535	50	801	1.560549	<b>3.70E+01</b>	ENST00000295754
8	<b><i>CALHM2</i></b>	171	7	35	5	<b>3.81E+01</b>	ENST00000393235
9	<b><i>LY86</i></b>	354	15	147	2.55102	<b>5.14E+01</b>	ENST00000230568
10	<b><i>AURKA</i></b>	805	23	285	2.017544	<b>5.98E+01</b>	ENST00000395907

The siRNA seed matches with 3'UTRs of all genes were compared between the top 200 and a control group of non-hits (screen ranks 12,001-17,000). The significance of enrichment was highest for *TGFBR2* (Fisher's exact test).

**Table S6.** *TGFBR2* is the only significantly off-targeted gene (both strands).

rank	gene	UTR length	count in hits	count in control	enrichment	p	Ensembl ID
1	<b><i>TGFBR2</i></b>	2535	128	1530	2.091503	<b>1.22E-11</b>	ENST00000295754
2	<i>CD248</i>	267	25	207	3.019324	1.20E-01	ENST00000311330
3	<i>C3orf52</i>	563	37	394	2.347716	1.45E-01	ENST00000480282
4	<i>TYMP</i>	500	35	377	2.320955	3.38E-01	ENST00000426603
5	<i>GALE</i>	345	29	288	2.517361	5.15E-01	ENST00000456977
6	<i>KCNC2</i>	1124	51	690	1.847826	1.24E+00	ENST00000298972
7	<i>KIF9</i>	255	25	241	2.593361	1.31E+00	ENST00000444589
8	<i>MAP3K13</i>	220	19	155	3.064516	1.55E+00	ENST00000454237
9	<i>PLEKHA6</i>	1567	76	1199	1.584654	2.06E+00	ENST00000272203
10	<i>SBF1</i>	391	27	283	2.385159	2.43E+00	ENST00000356279

The siRNA seed matches with 3'UTRs of all genes were compared between the top 200 and a control group of non-hits (screen ranks 12,001-17,000). The significance of enrichment was highest for *TGFBR2* (Fisher's exact test).

**Table S7.** *siRNA library composition (guide strand)*.

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
<b>A</b>	45.2%	18.6%	23.6%	24.7%	24.1%	22.9%	24.3%	23.2%	22.6%	26.0%	23.0%	23.0%	24.6%	24.0%	21.4%	22.7%	21.9%	21.8%	18.6%
<b>C</b>	2.9%	24.8%	25.7%	24.5%	24.6%	25.4%	24.5%	25.2%	26.8%	23.2%	25.4%	26.0%	24.7%	24.8%	27.1%	26.7%	26.6%	26.7%	31.5%
<b>G</b>	3.2%	30.1%	24.5%	23.2%	23.7%	25.5%	23.3%	24.6%	25.8%	22.7%	24.9%	25.6%	23.7%	24.3%	27.2%	26.1%	25.8%	26.4%	25.9%
<b>U</b>	48.7%	26.5%	26.2%	27.7%	27.6%	26.2%	27.9%	27.0%	24.9%	28.1%	26.8%	25.4%	27.0%	26.9%	24.4%	24.6%	25.7%	25.1%	24.0%

Average occurrence of the four nucleotides in each position of the siRNA guide strand. Positions 20 and 21 are dTdT overhangs in both strands.

#### Supplemental Web Material:

Selected, representative images at: [http://cbio.mskcc.org/tgf-beta\\_screen/](http://cbio.mskcc.org/tgf-beta_screen/)